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## ALIGNMENTS

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RESULT 1
 A46493
 metastasis suppressor KAI1 - human
 N;Alternate names: cell surface glycoprotein KAII; membrane protein R2, inducible; type C;Species: Homo sapiens (man)
C; Date: 18-Jun-1993 #sequence revision 09-Aug-1996 #text_change 22-Jun-1999
C; Accession: I38942; S16156; A46493
R; Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J. Science 268, 884-886, 1995
 A;Title: KAII, a metastasis suppressor gene for prostate cancer on human chromosome 11p1
A;Reference number: I38942; MUID:95273964; PMID:7754374
 A; Accession: I38942
 A; Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
A; Residues: 1-267 < RES:
A;Cross-references: EMBL:U20770; NID:g806805; PIDN:AAC50133.1; PID:g806806
R;Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Bur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolog A;Reference number: S16156; MUID:91153380; PMID:1842498
 A; Accession: S16156
 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-267 < GAU>
A;Residues: 1-267 <GAU>
A;Cross-references: EMBL:X53795; NID:g35832; PIDN:CAA37804.1; PID:g35833
A;Note: the authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, N.
J. Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leuk
D9, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
A; Residues: 1-239, 'MV', 242-267 <IMA>
A;Cross-references: GB:S48196; NID:g258294; PIDN:AAB23825.1; PID:g258295 A;Experimental source: T-cell line MOLT-4
 A; Note: sequence extracted from NCBI backbone (NCBIP:117149)
 C; Genetics
 A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A; (Tobs-Televisites: GDS: 13216; CMM: 100023
A; Map position: 11p11.2-11p11.2
C; Superfamily: CD9 antigen
C; Keywords: glycoprotein; transmembrane protein
F; 1-10/Domain: intracellular #status predicted < CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <TM1>
F;38-78/Domain: transmembrane #status predicted <TM2>
F;58-78/Domain: intracellular #status predicted <TM2>
F;84-108/Domain: transmembrane #status predicted <TM3-
F;84-108/Domain: extracellular #status predicted <TM3-
F;109-227/Domain: extracellular #status predicted <TM3-
 P;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
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F;253-265/Domain: intracellular #status predicted <CY3>F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted
  Query Match 24.3%; Score 321.5; DB 1; Length 267;
Best Local Similarity 28.2%; Pred. No. 1.8e-19;
Matches 73; Conservative 53; Mismatches 106; Indels 27; Gaps
          Db
         69 LFCLLGYIGIHNBIRWLLIVYAVLITWTFAVOVVLSAFIITKKBEVQQLWHDKIDFVISE 128
Qy
         Db
Qy
        129 YGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKKENSGQV--PCSC-----T 179
        DЪ
Qу
        180 KSTLRKWFCDEPLNAT------YLEGCENKISAWYNVNVLTLIGINFGLLTSBVF 228
        Db
Qv
        229 QVSLTVCFFKNIKNIIHAE 247
        : |::| :: :|:|
245 GMVLSICLCRH----VHSE 259
Db
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A;Cross-references: GB:M58485
R;Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, DNA Cell Biol. 9, 479-485, 1990
A;Title: Characterization of three abundant mRNAs from human A;Reference number: A35826; MUID:91025550; PMID:2171551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 09-Aug-1996 #text_change 08-Dec-2000
C;Date: 17-May-1996 #sequence_revision 09-Aug-1996 #text_change 08-Dec-2000
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C;Date: 19-May-2000 #sequence_revi
C;Accession: A59260
R;Todd, S.C.; Doctor, V.S.; Levy,
                                                                                                                                                                                     A;Cross-references: EMBL:X07982; NID:g34526; PIDN:CAA30792.1; PID:g34527
R;Metzelaar, M.U.; Wijngaard, P.L.U.; Peters, P.U.; Sixma, J.J.; Nieuwenhuis, H.K.; Clev J. Biol. Chem. 266, 3239-3245, 1990
A;Title: CD63 antigen. A novel lysosomal membrane glycoprotein, cloned by a screening pr A;Reference number: A39514; MUID:91131632; PMID:1993697
A;Accession: A39514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 185, 436-442, 1992
A;Title: Genomic structure of the ME491/CD63 antigen gene and functional analysis
A;Reference number: 138016; MUID:92287132; PMID:1599482
A;Accession: 138016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: I38016; S01418; A39514; B35826; A61177; A6117 R;Hotta, H.; Miyamoto, H.; Hara, I.; Takahashi, N.; Homma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanoma-associated antigen CD63 [validated] - human
N;Alternate names: antigen ME491; lysosomal membrane glycoprotein CD63; ME491/CD63
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C; Superfamily:
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A;Title: Sequences and expression of six new members of A;Reference number: A59258; MUID:98390278; PMID:9714763
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning and characterization of an antigen associated with early stace. A;Reference number: S01418; MUID:88210273; PMID:3365686
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Cancer Res.
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A; Residues: 1-238 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S01418
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                                                                                                                                     A; Residues: 1-238 <MET>
                                                                                                                                                           A; Molecule type: mRNA
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Best Local
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Blood 77, 121-132, 1991
A;Title: Characterization of a novel self-associating Mr 40,000 platelet glycoprotein.
A;Reference number: A61173; MUID:91084576; PMID:1984792
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A;Accession: A61177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;12-35/Domain: transmembrane #status predicted <TM1>F;36-51/Domain: extracellular #status predicted <EXI>F;36-76/Domain: transmembrane #status predicted <TM2>F;77-80/Domain: intracellular #status predicted <CY2>F;81-103/Domain: transmembrane #status predicted <CY3>
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A; Introns: 22/3; 85/3; 110/3; 142/3; 189/3; 217/3
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A;Residues: 2-8, 'X', 10-16, 'XX', 19-21 <HIL>
R;Residues: 2-8, 'X', 10-16, 'XX', 19-21 R;Mang, M.X.; Earley Jr., J.J.; Shields, J.A.; Donoso, L.A.
R;Wang, M.X.; Earley Jr., J.J.; Shields, J.A.; Donoso, L.A.
A;Tithe: An ocular melanoma-associated antigen. Molecular characterization.
A;Reference number: A56782; MUID:92181348; PMID:1339263
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A; Residues: 2-68, 'P', 70-238 <AZO>
R; Hildreth, J.E.K.; Derr, D.; Azo
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A;Note: the authors did not translate the codons for residues 205 throug
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;104-202/Domain: extracellular #status predicted <EX2>;203-228/Domain: transmembrane #status predicted <TM4>;229-238/Domain: intracellular #status predicted <CY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: CD9 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150,172/Binding site: carbohydrate
                                                                                                                                   176 CSCTKSTLRKWFCDEPLNATYLEGCENKISAWYNVNVLTLIGINFGLLTSEVFQVSLTVC
236 FFKNIKN 242
                                                                                                                                                                                                        112 MSEFNNNFRQQMENYPKNNHTASILDRMQADFKCCGAANYTDWEKIPSMSKNR--
                                                                                                                                                                                                                                                                         126 ISEYGS-----KDKPEDITKWTILNALQKTLQCCGQHNYTDWIK----NKNKENSGQVP 175
                                                                                                                                                                                                                                                                                                                                               65 FLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAAAIAGYVFRDK------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 VKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIIQGATPGS---LLPV--VIIAVGVFL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 IKYFLNLINGAF--LVLGLLFMGFGAWLLLDRNNFLTAFDENNHFIVPISQILIGMGSST 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-238 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    VLFCLLGYIGIHNEIRWLLIVYAVLITWTFAVQV--VLSAFIITKKEEVQQLWHDKIDFV 125
                                                                     DSCCINVTVGCGINFNEKAIHKEGCVEKIGGWLRKNVLVVAAAALGIAFVEVLGIVFACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.A.; Hildreth, J.E.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 202.5; DB 1;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (covalent) #status
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